

FIG. 1

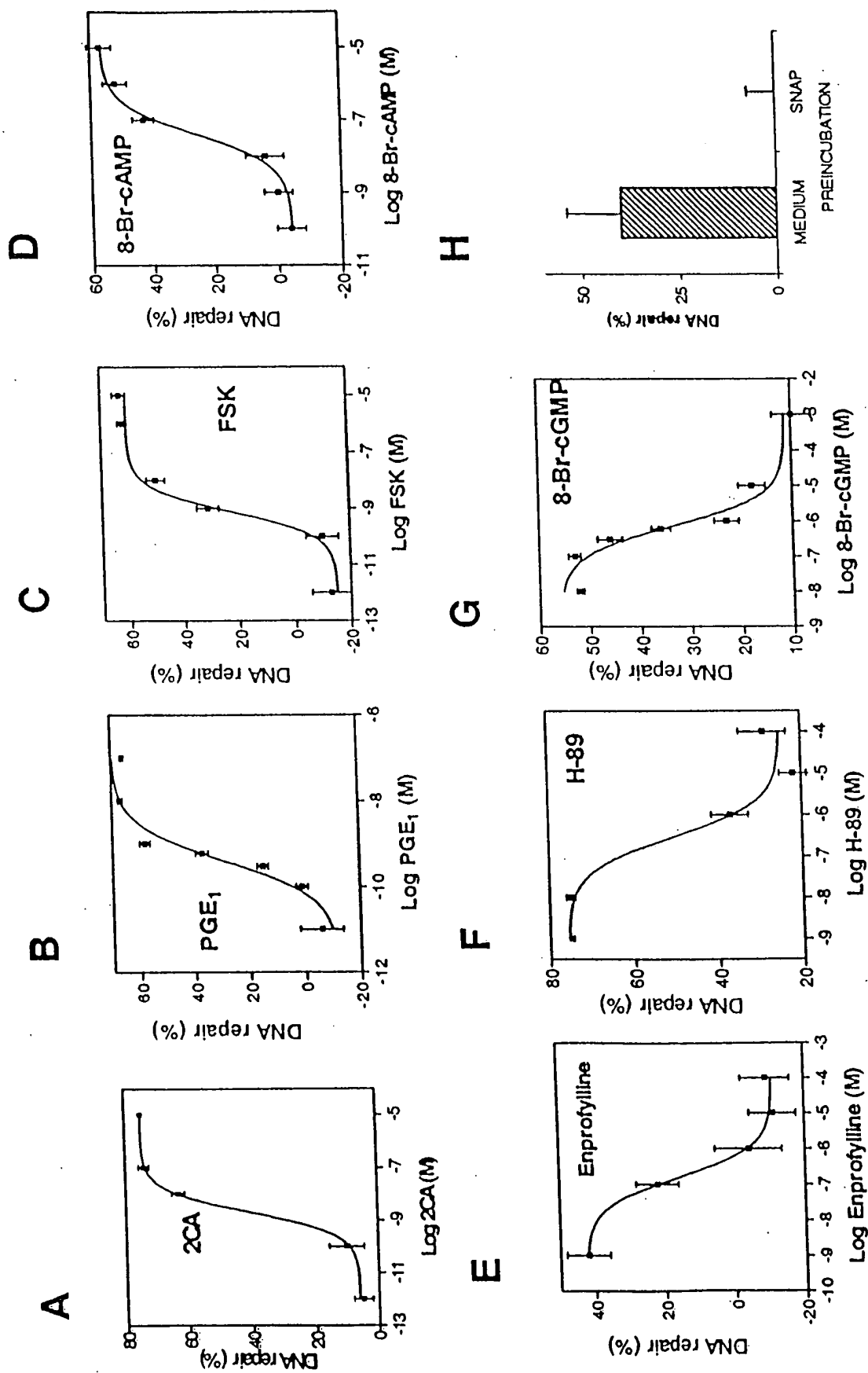


FIG. 2

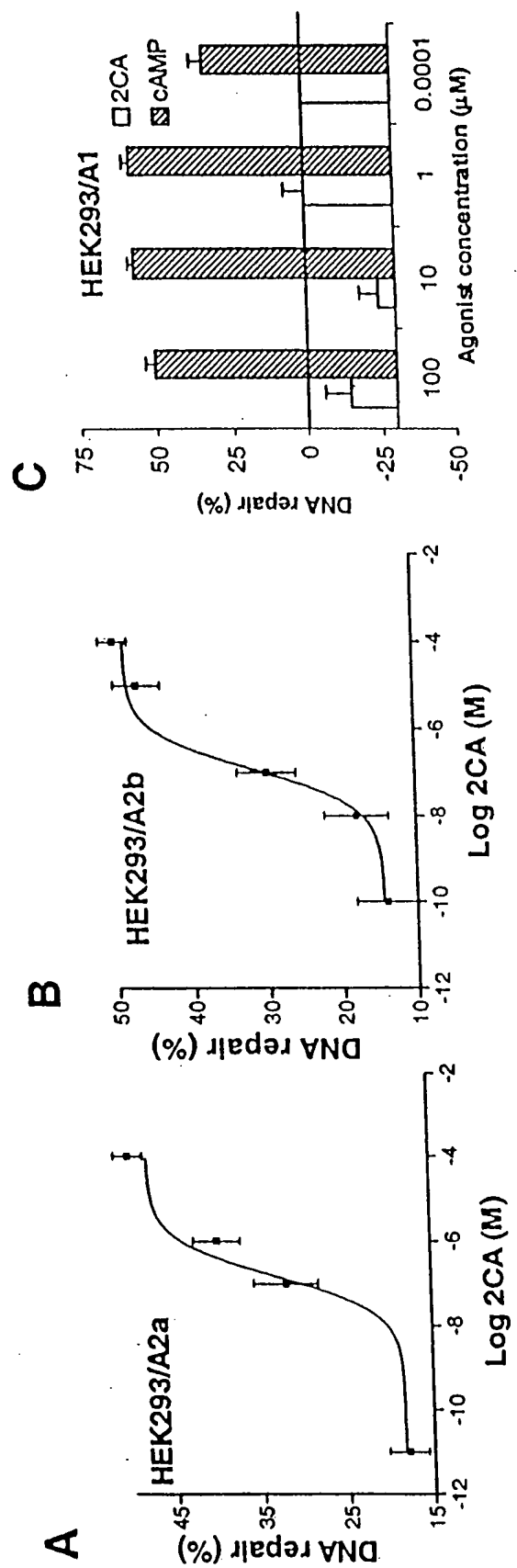


FIG. 3

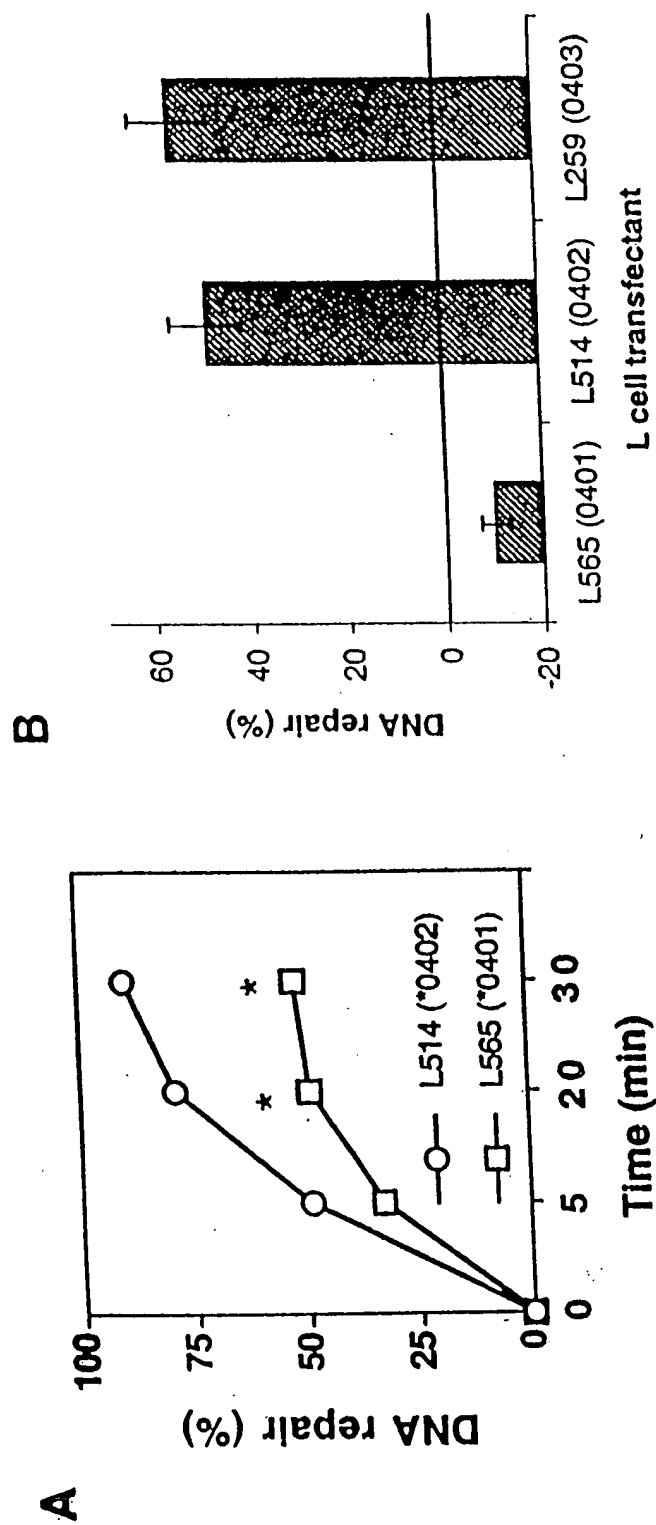


FIG. 4

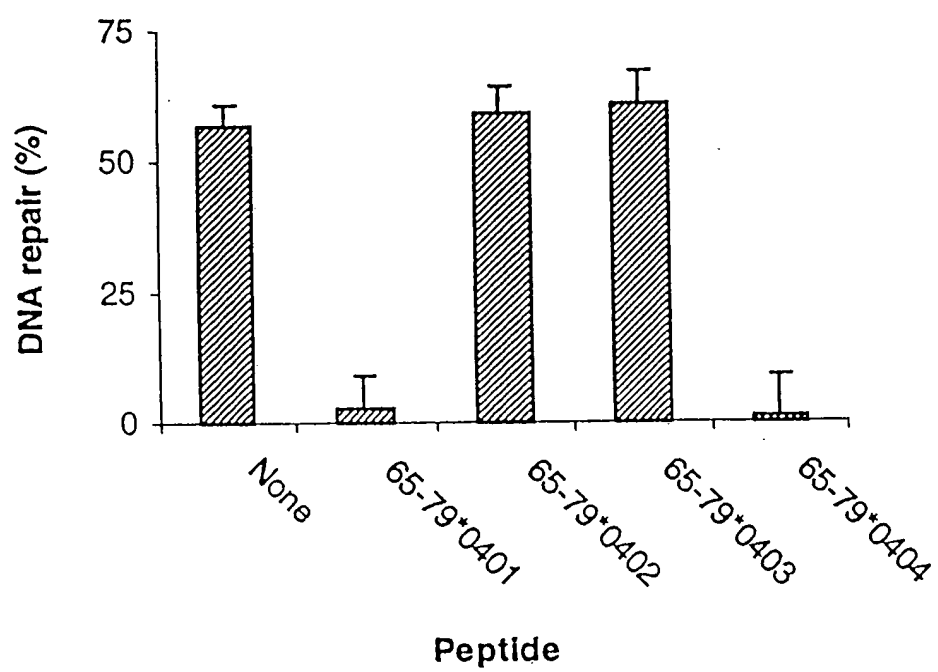


FIG. 5

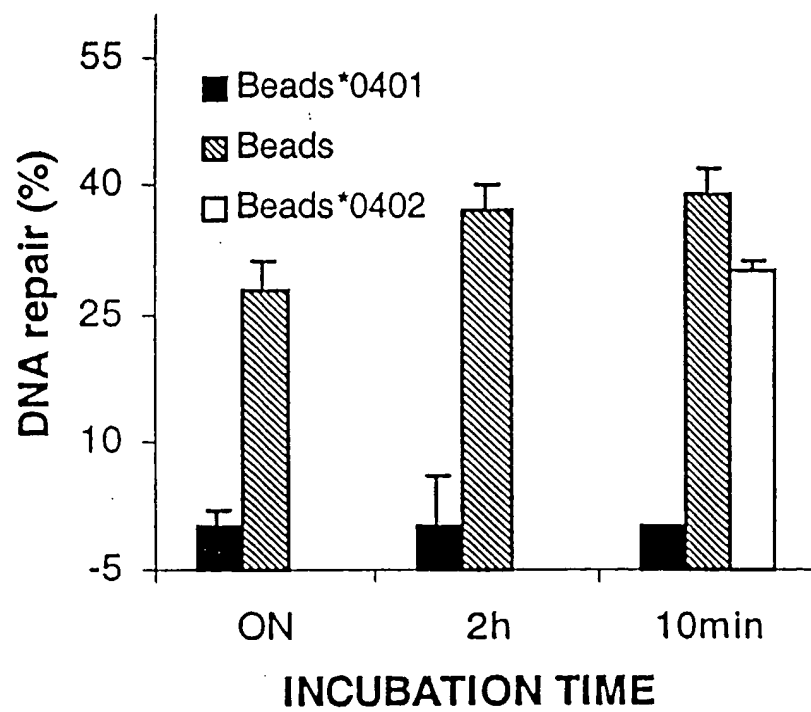


FIG. 6

HLA-DR β *0401	X _n QKRAAX _n	Xaa _n Gln Lys Arg Ala AlaXaa _n	[SEQ ID NO:28]
*0402	X _n DERAAX _n	Xaa _n Asp Glu Arg Ala AlaXaa _n	[SEQ ID NO:29]
*0403	X _n QRRRAEX _n	Xaa _n Gln Arg Arg Ala GluXaa _n	[SEQ ID NO:30]
*0404	X _n QRRRAAX _n	Xaa _n Gln Arg Arg Ala AlaXaa _n	[SEQ ID NO:31]
H. Laminin β 2	X _n QRRRAAX _n	Xaa _n Gln Arg Arg Ala AlaXaa _n	[SEQ ID NO:31]
M. Laminin β 2	X _n QRRRTAX _n	Xaa _n Gln Arg Arg Thr AlaXaa _n	[SEQ ID NO:32]
APLP1	X _n QRRRAAX _n	Xaa _n Gln Arg Arg Ala AlaXaa _n	[SEQ ID NO:31]
ApoE ϵ 4	X _n QKRLAX _n	Xaa _n Gln Lys Arg Leu AlaXaa _n	[SEQ ID NO:33]
ϵ 3	X _n QKRLAX _n	Xaa _n Gln Lys Arg Leu AlaXaa _n	[SEQ ID NO:33]
ϵ 2	X _n QKCLAX _n	Xaa _n Gln Lys Cys Leu AlaXaa _n	[SEQ ID NO:34]

FIG. 7

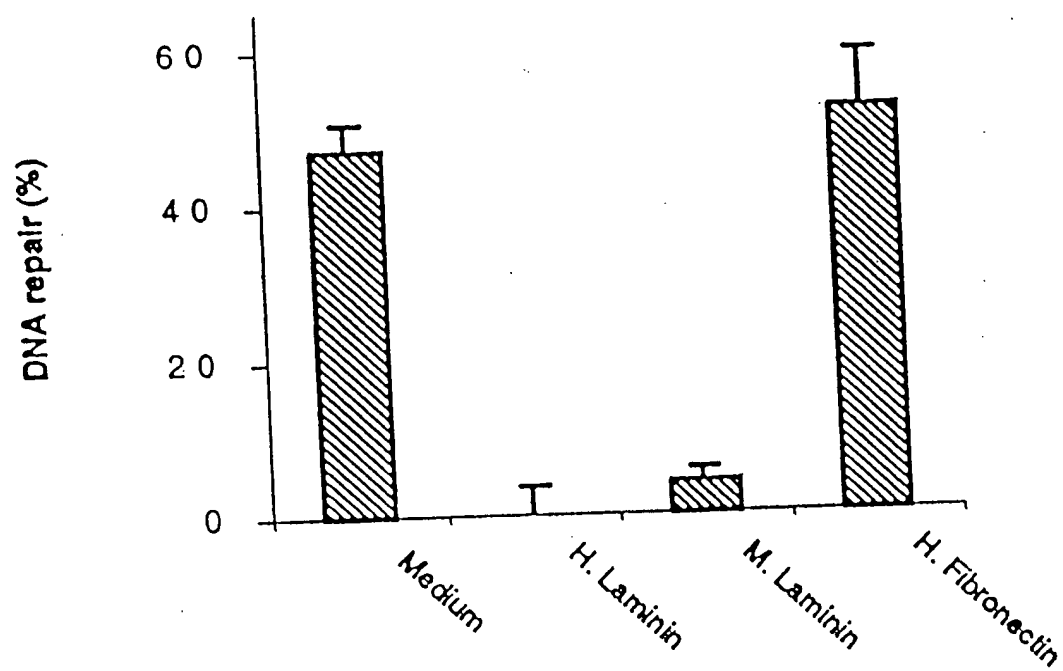


FIG. 8

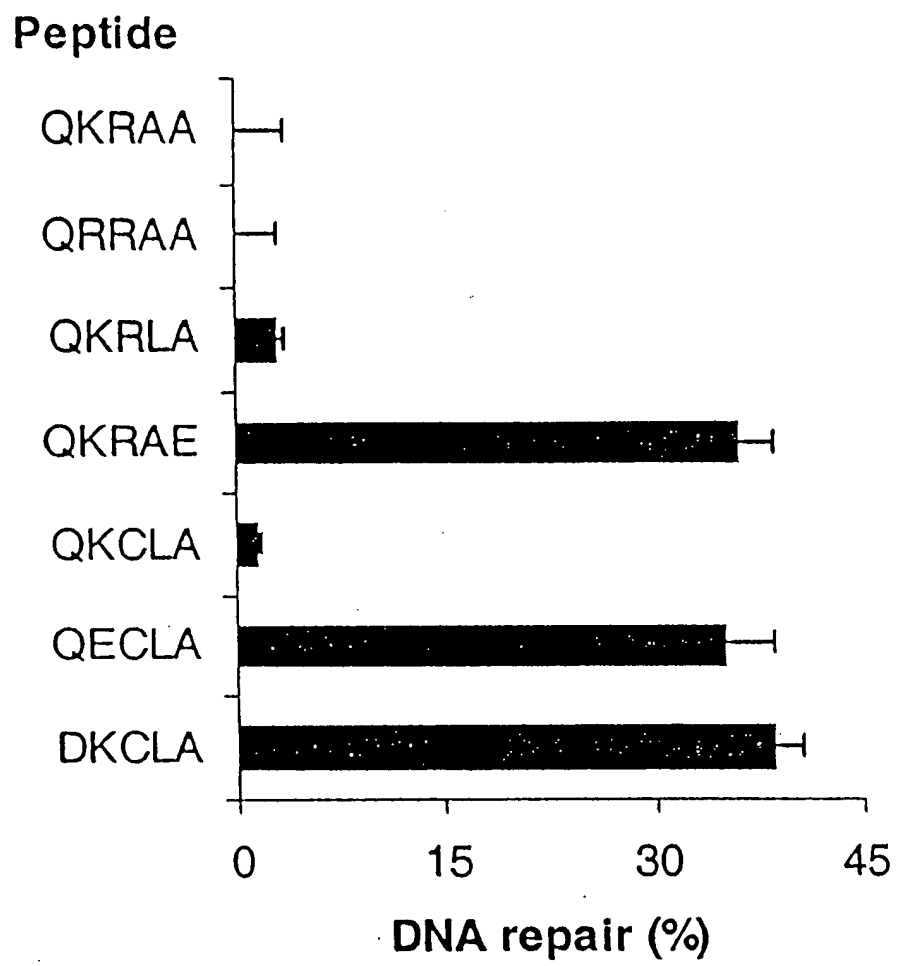
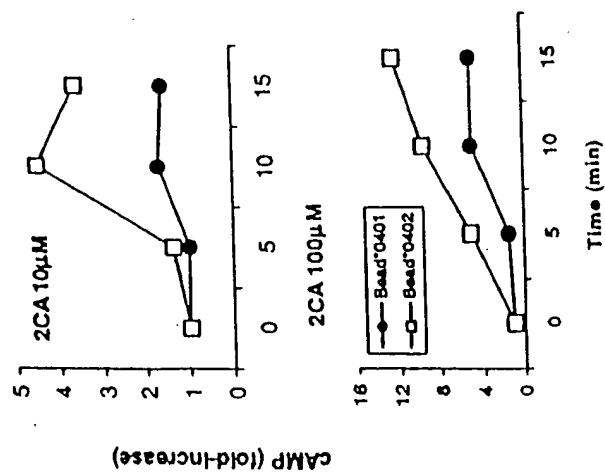


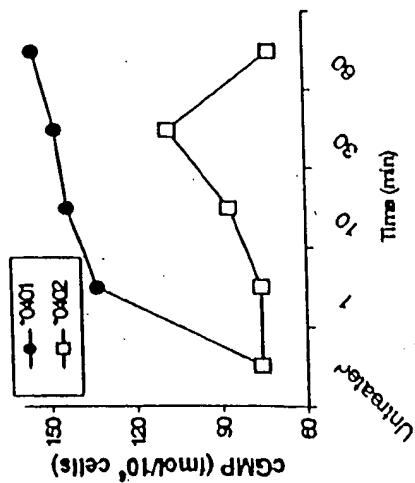
FIG. 9

FIG. 10

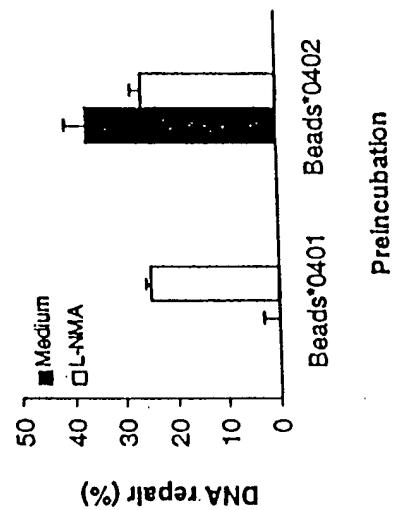
A



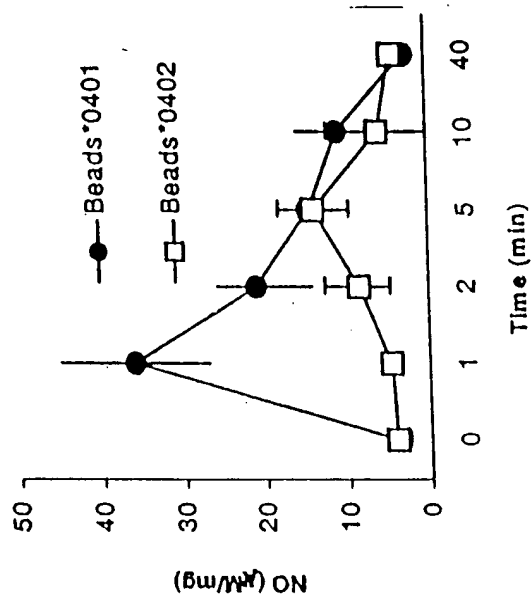
D



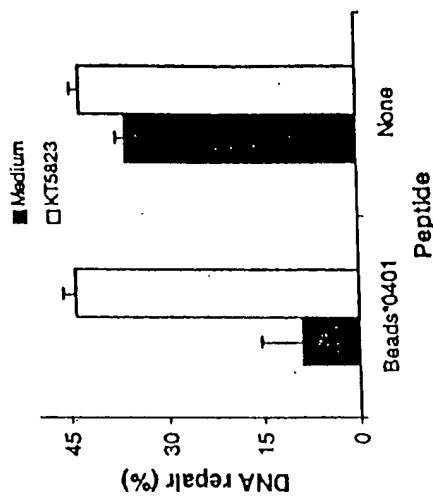
E



C



F



HBC*0401 [SEQ ID NO:17]

MDIDPYKEFGATVELLSFLPSDFFPSVRDLLDNASALYREALSPHHTALRQAILCWGELMTLATWVGNGLED

HKDLLEQKRAAVDTYCVDPISRDLVVSYYVNTNMGLKFRQLLWFHISCLTFGRETVIEYLVSGVWIRTTPPAYRPPNAP

ILSTLPARVIN

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu Pro
Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Asn Ala Ser Ala Leu Tyr Arg Glu
Ala Leu Glu Ser Pro Glu His Cys Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu
Cys Trp Gly Glu Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp His Lys
Asp Leu Leu Glu Gln Lys Arg Ala Ala Val Asp Thr Tyr Cys Val Asp Pro Ile Ser Arg
Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln Leu Leu Trp
Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val Ile Glu Tyr Leu Val Ser Phe
Gly Val Trp Ile Arg Thr Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr
Leu Pro Ala Trp Ala Arg Val Ile Asn

FIG. 11 A

HBC*0402 [SEQ ID NO:18]

MDIDPYKEFGATVELLSFLPSDFPSPVRDLLDNASALYREALSPHHTALRQAILCWGELMTLATWVGNNLED

HKDILEDERAADVTCVDPISRDLVVSYYVNTNMGLKFRQLLWFHISCLTFGRETVIEYLVSGVWIRTPPAYRPPNAP

ILSTLPARVIN

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu Pro
Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Asn Ala Ser Ala Leu Tyr Arg Glu
Ala Leu Glu Ser Pro Glu His Cys Ser Pro His Thr Ala Leu Arg Gln Ala Ile Leu
Cys Trp Gly Glu Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp His Lys
Asp Ile Leu Glu Asp Glu Arg Ala Ala Val Asp Thr Tyr Cys Val Asp Pro Ile Ser Arg
Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln Leu Leu Trp
Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val Ile Glu Tyr Leu Val Ser Phe
Gly Val Trp Ile Arg Thr Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr
Leu Pro Ala Trp Ala Arg Val Ile Asn

FIG. 11 A Cont.

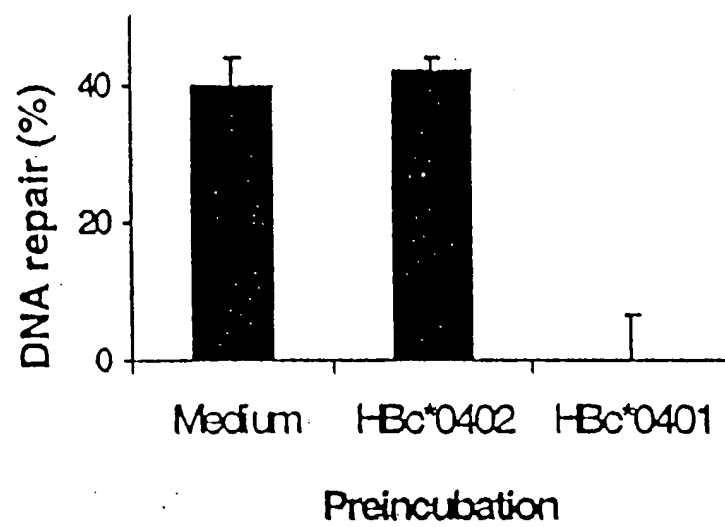


FIG. 11B

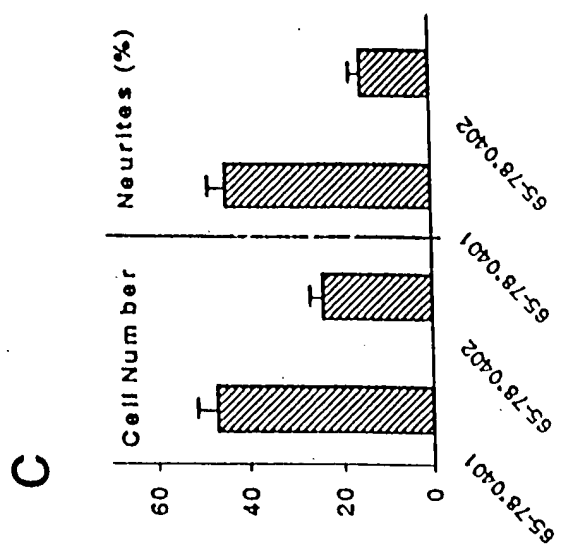


FIG. 12

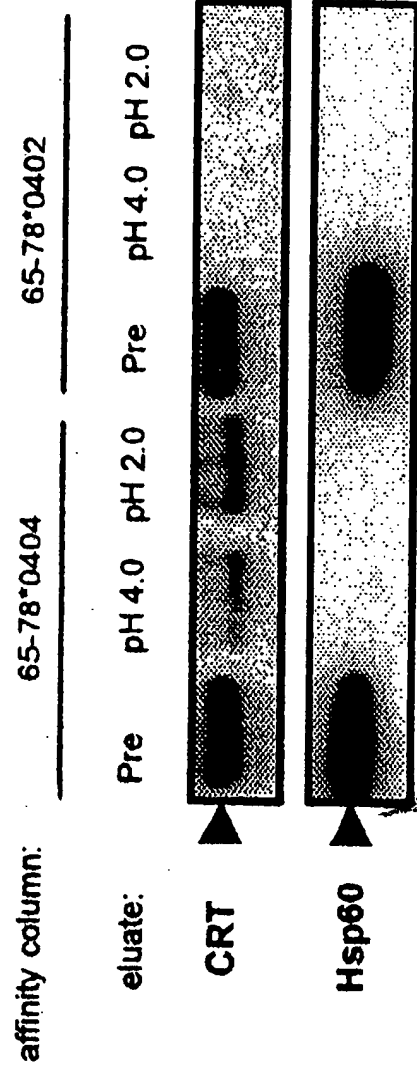


FIG. 13A

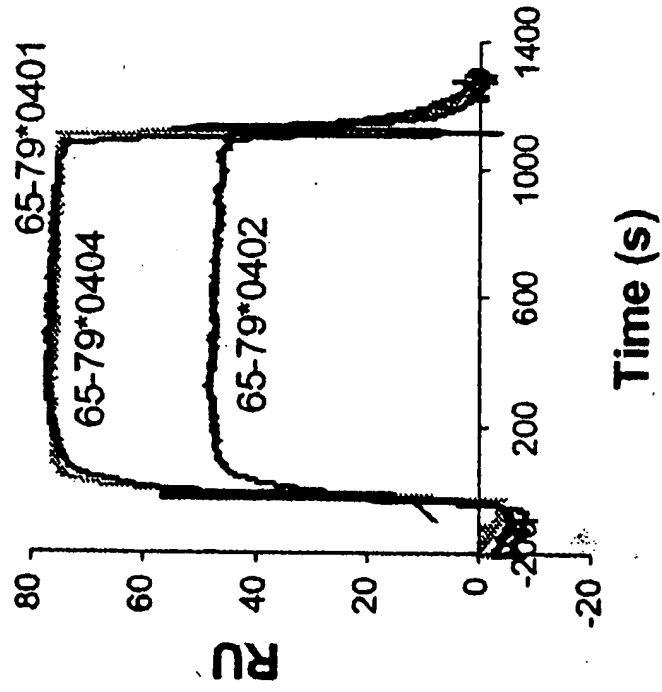


FIG. 13B

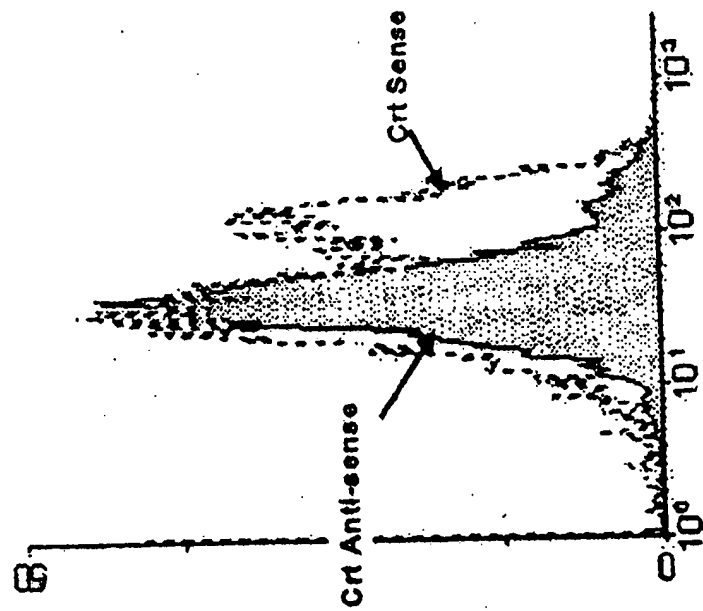


FIG. 13C

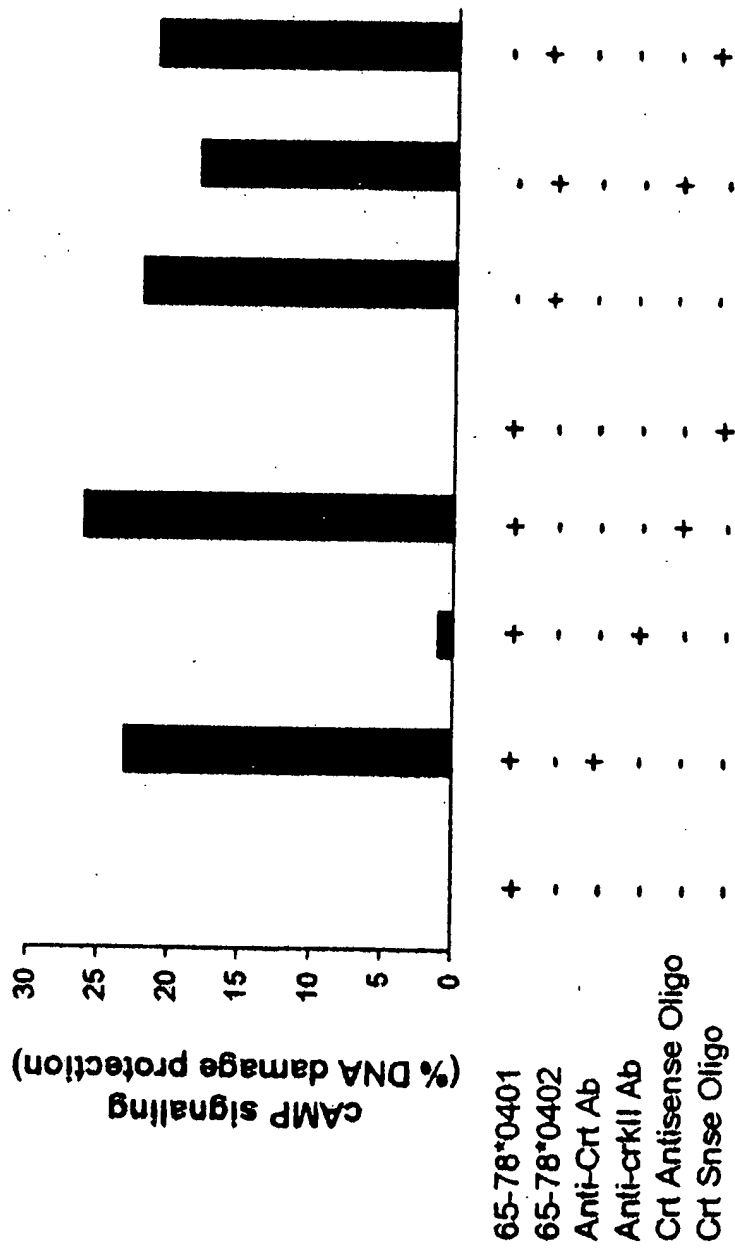


FIG. 13D

1 mllsvplllg llglavaepa vyfkeqfldg dgwtsrwies khksdfgkfv lssgkfygde
61 ekdkglqtsq darfyalsas fepfsnkgqt lvvqftvkhe qnidcgggyv klfpnsldqt
121 dmhgdseyni mfgpdicgpg tkkvhvifny kgknvlinkd ircdddefth lytlivrpdn
181 tyevkidnsq vesgsleddw dflppkkikd pdaskpedwd erakiddptd skpedwdkpe
241 hipdpdakkp edwdeemdge weppvignpe ykgewkprqi dnpdykgtwi hpeidnpeys
301 pdpsiyaydn fgvlglldlwq vksgtifdnf litndeayae efgnetwgtv kaaekqmkdk
361 qdeeqrlkee eedkkrkeee eaedkedded kdedeedeed keedeedvp ggakdel

FIG. 14